

MAY 07 2002

SEQUENCE LISTING

<110> Li, Jing
Powers, Scott
Xiang, Phil
Peng, Yue
Tularik Inc.

<120> PRC17: An Amplified Cancer Gene

<130> 018781-007610US

<140> US 10/071,838

<141> 2001-02-08

<150> US 60/267,615

<151> 2001-02-08

<160> 18

<170> PatentIn Ver. 2.1

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<211> 1964

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<221> CDS

<222> (1)..(1650)

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35 40 45
Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
50 55 60
Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
65 70 75 80
Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
85 90 95
Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
100 105 110
Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
115 120 125
Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
130 135 140
Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
145 150 155 160
Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
165 170 175
Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
180 185 190
Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
195 200 205
Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
210 215 220

His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
 225 230 235 240
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys
 245 250 255
 Lys Asp Leu Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile
 260 265 270
 Leu Ile Asp Gly Ile Ser Leu Gly Leu Thr Leu Arg Leu Trp Asp Val
 275 280 285
 Tyr Leu Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala
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 Phe Lys Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro
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 Trp Ala Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu
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 Lys Gln Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser
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 Gly Asp Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro
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 405 410 415
 Pro Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly
 420 425 430
 Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
 435 440 445
 Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
 450 455 460
 Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
 465 470 475 480
 Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
 485 490 495
 His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
 500 505 510
 Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala
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<212> DNA
<213> Homo sapiens

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<223> human PRC17 splice variant 1 (exon 3 expanded)

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<221> CDS
<222> (1)..(1832)

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35 40 45
Leu Gly Ile Val Gln Ser Cys Arg Ser Trp Glu Ser Ala Pro Gln Glu
50 55 60
Gly Pro Cys Pro Pro Phe Pro Val Pro Ser Pro Gly Leu Ser Pro Glu
65 70 75 80
Leu Glu Arg Asp Arg Ala Ser Pro Phe Trp Gly Ser Ala Pro Arg Leu
85 90 95
Gly Pro Leu Gln Ala Pro Cys Ser Ser Ser Ala Leu Pro Gly Leu Pro
100 105 110
Tyr Ser Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu Ala Lys Gln
115 120 125
Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp Met Leu Gly
130 135 140
Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp Arg Ala Tyr
145 150 155 160
Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser Val Leu Leu
165 170 175
Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr Gln Ile Met
180 185 190
Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg Ile Asp Arg
195 200 205
Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg Asp Arg Tyr
210 215 220
Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala Tyr Glu Glu
225 230 235 240
Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His Ile Ala Ala
245 250 255
Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp Ala Leu Val
260 265 270
Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe His Ser Pro
275 280 285
Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu His Val Val
290 295 300

Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Asp Lys Lys Asp Leu
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 Cys Gly Gln Cys Ser Pro Leu Gly Cys Leu Ile Arg Ile Leu Ile Asp
 325 330 335
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 355 360 365
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 370 375 380
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 385 390 395 400
 Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln Gly
 405 410 415
 Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser Arg
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 Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp Arg
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 <212> DNA
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 <222> (1)..(1538)

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 <213> Homo sapiens

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 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
 165 170 175
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
 180 185 190
 Ile Ala Ala Leu Phe Leu Leu Tyr Leu Pro Glu Glu Asp Ala Phe Trp
 195 200 205
 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
 210 215 220
 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
 225 230 235 240
 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Tyr Leu
 245 250 255
 Val Glu Gly Glu Gln Ala Leu Met Pro Ile Thr Arg Ile Ala Phe Lys
 260 265 270
 Val Gln Gln Lys Arg Leu Thr Lys Thr Ser Arg Cys Gly Pro Trp Ala
 275 280 285
 Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr
 290 295 300
 Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln
 305 310 315 320
 Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser
 325 330 335
 Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp
 340 345 350

Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp
 355 360 365
 Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly
 370 375 380
 Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro
 385 390 395 400
 Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu
 405 410 415
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 420 425 430
 Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val Arg Ala
 435 440 445
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 450 455 460
 Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp
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<220>
 <223> Description of Artificial Sequence:forward primer
 for PCR amplification of PRC17 cDNA

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22

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:reverse primer
 for PCR amplification of PRC17 cDNA

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21

<210> 9
<211> 20
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<213> Artificial Sequence

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Sequence:fluorescent-labeled PCR TaqMan detection
probe for PRC17

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<222> (1)
<223> n = Fam-labeled t

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<222> (20)
<223> n = TAMRA-labeled g

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20

<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer
for full-length PRC17 splice variant 1 cDNA
isolation

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18

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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for full-length PRC17 splice variant 1 cDNA
isolation

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19

<210> 12
<211> 29
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<220>
<223> Description of Artificial Sequence:PCR TaqMan
detection probe for PRC17 splice variant 1

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<221> modified_base
<222> (1)
<223> n = Fam-labeled t

<220>
<221> modified_base
<222> (29)
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<400> 12
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29

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope
tag

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1 5

<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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epitope tag

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1 5

<210> 15
<211> 200
<212> PRT
<213> Artificial Sequence

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flexible linker

<220>
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<222> (6)..(200)
<223> Gly at positions 6-200 may be present or absent

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1 5 10 15

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 50 55 60
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 65 70 75 80
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 85 90 95
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 115 120 125
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 145 150 155 160
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 195 200

<210> 16
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unique PRC17
 C-terminal peptide

<400> 16
 Pro Ser Thr Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln
 1 5 10 15

Pro Cys

<210> 17
 <211> 786
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human TRE-2/USP6

<400> 17

Met	Asp	Met	Val	Glu	Asn	Ala	Asp	Ser	Leu	Gln	Ala	Gln	Glu	Arg	Lys	1	5	10	15
Asp	Ile	Leu	Met	Lys	Tyr	Asp	Lys	Gly	His	Arg	Ala	Gly	Leu	Pro	Glu	20	25	30	
Asp	Lys	Gly	Pro	Glu	Pro	Val	Gly	Ile	Asn	Ser	Ser	Ile	Asp	Arg	Phe	35	40	45	
Gly	Ile	Leu	His	Glu	Thr	Glu	Leu	Pro	Pro	Val	Thr	Ala	Arg	Glu	Ala	50	55	60	
Lys	Lys	Ile	Arg	Arg	Glu	Met	Thr	Arg	Thr	Ser	Lys	Trp	Met	Glu	Met	65	70	75	80
Leu	Gly	Glu	Trp	Glu	Thr	Tyr	Lys	His	Ser	Ser	Lys	Leu	Ile	Asp	Arg	85	90	95	
Val	Tyr	Lys	Gly	Ile	Pro	Met	Asn	Ile	Arg	Gly	Pro	Val	Trp	Ser	Val	100	105	110	
Leu	Leu	Asn	Ile	Gln	Glu	Ile	Lys	Leu	Lys	Asn	Pro	Gly	Arg	Tyr	Gln	115	120	125	
Ile	Met	Lys	Glu	Arg	Gly	Lys	Arg	Ser	Ser	Glu	His	Ile	His	His	Ile	130	135	140	
Asp	Leu	Asp	Val	Arg	Thr	Thr	Leu	Arg	Asn	His	Val	Phe	Phe	Arg	Asp	145	150	155	160
Arg	Tyr	Gly	Ala	Lys	Gln	Arg	Glu	Leu	Phe	Tyr	Ile	Leu	Leu	Ala	Tyr	165	170	175	
Ser	Glu	Tyr	Asn	Pro	Glu	Val	Gly	Tyr	Cys	Arg	Asp	Leu	Ser	His	Ile	180	185	190	
Thr	Ala	Leu	Phe	Leu	Leu	Tyr	Leu	Pro	Glu	Glu	Asp	Ala	Phe	Trp	Ala	195	200	205	
Leu	Val	Gln	Leu	Leu	Ala	Ser	Glu	Arg	His	Ser	Leu	Pro	Gly	Phe	His	210	215	220	
Ser	Pro	Asn	Gly	Gly	Thr	Val	Gln	Gly	Leu	Gln	Asp	Gln	Gln	Glu	His	225	230	235	240
Val	Val	Pro	Lys	Ser	Gln	Pro	Lys	Thr	Met	Trp	His	Gln	Asp	Lys	Glu	245	250	255	
Gly	Leu	Cys	Gly	Gln	Cys	Ala	Ser	Leu	Gly	Cys	Leu	Leu	Arg	Asn	Leu	260	265	270	
Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Thr	Leu	Arg	Leu	Trp	Asp	Val	Tyr	275	280	285	
Leu	Val	Glu	Gly	Glu	Gln	Val	Leu	Met	Pro	Ile	Thr	Ser	Ile	Ala	Leu	290	295	300	
Lys	Val	Gln	Gln	Lys	Arg	Leu	Met	Lys	Thr	Ser	Arg	Cys	Gly	Leu	Trp	305	310	315	320

Ala Arg Leu Arg Asn Gln Phe Phe Asp Thr Trp Ala Met Asn Asp Asp
 325 330 335
 Thr Val Leu Lys His Leu Arg Ala Ser Thr Lys Lys Leu Thr Arg Lys
 340 345 350
 Gln Gly Asp Leu Pro Pro Pro Ala Lys Arg Glu Gln Gly Ser Leu Ala
 355 360 365
 Pro Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly
 370 375 380
 Tyr Arg Gln Ala Pro Pro Gly Pro Pro Ala Gln Phe Gln Arg Pro Ile
 385 390 395 400
 Cys Ser Ala Ser Pro Pro Trp Ala Ser Arg Phe Ser Thr Pro Cys Pro
 405 410 415
 Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val
 420 425 430
 Pro Ser Leu Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe
 435 440 445
 Leu Glu Trp Lys Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Ile Gly
 450 455 460
 Gly Pro Trp Phe Pro His Tyr Asp Phe Glu Arg Ser Cys Trp Val Arg
 465 470 475 480
 Ala Ile Ser Gln Glu Asp Gln Leu Ala Thr Cys Trp Gln Ala Glu His
 485 490 495
 Cys Gly Glu Val His Asn Lys Asp Met Ser Trp Pro Glu Glu Met Ser
 500 505 510
 Phe Thr Ala Asn Ser Ser Lys Ile Asp Arg Gln Lys Val Pro Thr Glu
 515 520 525
 Lys Gly Ala Thr Gly Leu Ser Asn Leu Gly Asn Thr Cys Phe Met Asn
 530 535 540
 Ser Ser Ile Gln Cys Val Ser Asn Thr Gln Pro Leu Thr Gln Tyr Phe
 545 550 555 560
 Ile Ser Gly Arg His Leu Tyr Glu Leu Asn Arg Thr Asn Pro Ile Gly
 565 570 575
 Met Lys Gly His Met Ala Lys Cys Tyr Gly Asp Leu Val Gln Glu Leu
 580 585 590
 Trp Ser Gly Thr Gln Lys Ser Val Ala Pro Leu Lys Leu Arg Arg Thr
 595 600 605
 Ile Ala Lys Tyr Ala Pro Lys Phe Asp Gly Phe Gln Gln Gln Asp Ser
 610 615 620
 Gln Glu Leu Leu Ala Phe Leu Leu Asp Gly Leu His Glu Asp Leu Asn
 625 630 635 640

Arg Val His Glu Lys Pro Tyr Val Glu Leu Lys Asp Ser Asp Gly Arg
 645 650 655
 Pro Asp Trp Glu Val Ala Ala Glu Ala Trp Asp Asn His Leu Arg Arg
 660 665 670
 Asn Arg Ser Ile Ile Val Asp Leu Phe His Gly Gln Leu Arg Ser Gln
 675 680 685
 Val Lys Cys Lys Thr Cys Gly His Ile Ser Val Arg Phe Asp Pro Phe
 690 695 700
 Asn Phe Leu Ser Leu Pro Leu Pro Met Asp Ser Tyr Met Asp Leu Glu
 705 710 715 720
 Ile Thr Val Ile Lys Leu Asp Gly Thr Thr Pro Val Arg Tyr Gly Leu
 725 730 735
 Arg Leu Asn Met Asp Glu Lys Tyr Thr Gly Leu Lys Lys Gln Leu Arg
 740 745 750
 Asp Leu Cys Gly Leu Asn Ser Glu Gln Ile Leu Leu Ala Glu Val His
 755 760 765
 Asp Ser Asn Ile Lys Ile Ser Pro Leu His His Leu Gln Met Glu Cys
 770 775 780
 Ser Pro
 785

<210> 18
 <211> 549
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human PRC17.codi

<400> 18
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 Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
 20 25 30
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110

Val	Leu	Leu	Asn	Ile	Glu	Glu	Met	Lys	Leu	Lys	Asn	Pro	Gly	Arg	Tyr		
		115					120					125					
Gln	Ile	Met	Lys	Glu	Lys	Gly	Lys	Arg	Ser	Ser	Glu	His	Ile	Gln	Arg		
		130				135					140						
Ile	Asp	Arg	Asp	Ile	Ser	Gly	Thr	Leu	Arg	Lys	His	Met	Phe	Phe	Arg		
		145			150					155					160		
Asp	Arg	Tyr	Gly	Thr	Lys	Gln	Arg	Glu	Leu	Leu	His	Ile	Leu	Leu	Ala		
				165					170					175			
Tyr	Glu	Glu	Tyr	Asn	Pro	Glu	Val	Gly	Tyr	Cys	Arg	Asp	Leu	Ser	His		
			180					185					190				
Ile	Ala	Ala	Leu	Phe	Leu	Leu	Tyr	Leu	Pro	Glu	Glu	Asp	Ala	Phe	Trp		
		195					200					205					
Ala	Leu	Val	Gln	Leu	Leu	Ala	Ser	Glu	Arg	His	Ser	Leu	Gln	Gly	Phe		
		210				215					220						
His	Ser	Pro	Asn	Gly	Gly	Thr	Val	Gln	Gly	Leu	Gln	Asp	Gln	Gln	Glu		
		225			230					235					240		
His	Val	Val	Ala	Thr	Ser	Gln	Ser	Lys	Thr	Met	Gly	His	Gln	Asp	Lys		
			245					250						255			
Lys	Asp	Leu	Cys	Gly	Gln	Cys	Ser	Pro	Leu	Gly	Cys	Leu	Ile	Arg	Ile		
		260						265					270				
Leu	Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Thr	Leu	Arg	Leu	Trp	Asp	Val		
		275					280					285					
Tyr	Leu	Val	Glu	Gly	Glu	Gln	Ala	Leu	Met	Pro	Ile	Thr	Arg	Ile	Ala		
		290				295					300						
Phe	Lys	Val	Gln	Gln	Lys	Arg	Leu	Thr	Lys	Thr	Ser	Arg	Cys	Gly	Pro		
		305			310					315					320		
Trp	Ala	Arg	Phe	Cys	Asn	Arg	Phe	Val	Asp	Thr	Trp	Ala	Arg	Asp	Glu		
				325					330					335			
Asp	Thr	Val	Leu	Lys	His	Leu	Arg	Ala	Ser	Met	Lys	Lys	Leu	Thr	Arg		
			340					345					350				
Lys	Gln	Gly	Asp	Leu	Pro	Pro	Pro	Ala	Lys	Pro	Glu	Gln	Gly	Ser	Ser		
		355					360					365					
Ala	Ser	Arg	Pro	Val	Pro	Ala	Ser	Arg	Gly	Gly	Lys	Thr	Leu	Cys	Lys		
		370				375					380						
Gly	Asp	Arg	Gln	Ala	Pro	Pro	Gly	Pro	Pro	Ala	Arg	Phe	Pro	Arg	Pro		
		385			390					395					400		
Ile	Trp	Ser	Ala	Ser	Pro	Pro	Arg	Ala	Pro	Arg	Ser	Ser	Thr	Pro	Cys		
				405					410					415			
Pro	Gly	Gly	Ala	Val	Arg	Glu	Asp	Thr	Tyr	Pro	Val	Gly	Thr	Gln	Gly		
			420				425						430				

Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
435 440 445

Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
450 455 460

Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
465 470 475 480

Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
485 490 495

His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
500 505 510

Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Gln Tyr Ala
515 520 525

Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
530 535 540

Q' core Phe Pro Pro Gly Phe
545